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#38

RAW SEQUENCE LISTING

DATE: 08/07/2002

PATENT APPLICATION: US/08/403,803C

TIME: 10:24:18

Input Set : A:\1747-41426-A-PCT-US.txt

Output Set: N:\CRF3\08072002\H403803C.raw

ENTERED

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3 <110> APPLICANT: Ron S., Israeli et al.
5 <120> TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN
7 <130> FILE REFERENCE: 1769/41426-A-PCT-US/JPW/MAF/DJK
9 <140> CURRENT APPLICATION NUMBER: US 08/403,803C
10 <141> CURRENT FILING DATE: 1995-03-17
12 <150> PRIOR APPLICATION NUMBER: PCT/US93/10624
13 <151> PRIOR FILING DATE: 1993-11-05
15 <160> NUMBER OF SEQ ID NOS: 38
17 <170> SOFTWARE: PatentIn version 3.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 2653
21 <212> TYPE: DNA
22 <213> ORGANISM: Human
24 <400> SEQUENCE: 1
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27 attggttcag tgcactctag aaacactgct gtggtggaga aactggaccc caggtctgga 120
29 gogaattcca gcctgcaggg ctgataagcg aggcattagt gagattgaga gagactttac 180
31 cccgcgcgtg tggttgagg ggcgcgagta gagcagcagc acaggcgcgg gtcccgggag 240
33 cccggtctctg ctgcgcgcga gatgtggaat ctccctcacg aaaccgactc ggcgtgtggc 300
35 accgcgcgcc gccgcgcgtg gctgtgcgct ggggcgcgtg tgctggcggg tggcttcttt 360
37 ctccctcggt tccctctcgg gtggtttata aaatcctcca atgaagctac taacattact 420
39 ccaaagcata atatgaaagc atttttggtt gaattgaaag ctgagaacat caagaagttc 480
41 ttatataatt ttacacagat accacattta gcaggaaacg aacaaaactt tcagcttgca 540
43 aagcaaatte aatcccagtg gaaagaattt ggccctggatt ctggtgagct agcacattat 600
45 gatgtcctgt tgtcctaccc aaataagact catcccaact acatctcaat aattaatgaa 660
47 gatggaaatg agattttcaa cacatcatta tttgaaccac ctccctccagg atatgaaaat 720
49 gtttcggata ttgtaccacc tttcagtgtt ttctctctc aaggaatgcc agaggcgcat 780
51 ctagtgtatg ttaactatgc acgaactgaa gacttcttta aattggaacg ggacatgaaa 840
53 atcaattgct ctgggaaaat tgtaattgcc agatatggga aagttttcag aggaaataag 900
55 gttaaaaaatg ccagctggc aggggccaaa ggagtcattc tctactccga cctgctgac 960
57 tactttgtct ctggggtgaa gtcctatcca gatggttgga atcttctctg aggtggtgtc 1020
59 cagcgtggaa atatcctaaa tctgaatggt gcaggagacc ctctcacacc aggttaccga 1080
61 gcaaatgaat atgcttatag gcgtggaatt gcagggctg ttggtcttcc aagtattcct 1140
63 gttcatccaa ttggatacta tgatgcacag aagctcctag aaaaaatggg tggctcagca 1200
65 ccaccagata gcagctggag aggaagtctc aaagtgcctt acaatgttgg acctggcttt 1260
67 actggaaact tttctacaca aaaagtcaag atgcacatcc actctacca tgaagtgaca 1320
69 agaatttaca atgtgatagg tactctcaga ggagcagtg aaccagacag atatgtcatt 1380
71 ctggggaggtc accgggactc atgggtgttt ggtggtattg accctcagag tggagcagct 1440
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75 agaacaattt tgtttgcaag ctgggatgca gaagaatttg gtcttcttgg ttctactgag 1560
77 tgggcagagg agaattcaag actccttcaa gagcgtggcg tggcttatat taatgctgac 1620
79 tcatctatag aaggaaacta cactctgaga gttgattgta caccgctgat gtacagcttg 1680
81 gtacacaacc taacaaaaga gctgaaaagc cctgatgaag gctttgaagg caaatctctt 1740

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83 tatgaaagtt ggactaaaaa aagtccttcc ccagagttca gtggcatgcc caggataagc 1800
85 aaattgggat ctggaaatga ttttgagggtg ttcttccaac gacttggaat tgcttcaggc 1860
87 agagcacggt atactaaaaa ttgggaaaca aacaaattca gcgctatcc actgtatcac 1920
89 agtgtctatg aaacatatga gttggtggaa aagttttatg atccaatgtt taaatatcac 1980
91 ctactgtggg cccaggttcg aggagggatg gtggttgagc tagccaattc catagtgtct 2040
93 ccttttgatt gtcgagatta tgctgtagtt ttaagaaagt atgctgacaa aatctacagt 2100
95 atttctatga aacatccaca ggaaatgaag acatacagtg tatcatttga ttcacttttt 2160
97 tctgcagtaa agaattttac agaaattgct tccaagttca gtgagagact ccaggacttt 2220
99 gacaaaagca acccaatagt attaagaatg atgaatgatc aactcatgtt tctggaaaga 2280
101 gcattttattg atccattagg gttaccagac aggccttttt ataggcatgt catctatgct 2340
103 ccaagcagcc acaacaagta tgcaggggag tcattcccag gaatttatga tgctctgttt 2400
105 gatattgaaa gcaaagtgga cccttccaag gcctggggag aagtgaagag acagatttat 2460
107 gttgcagcct tcacagtgcg ggcagctgca gagactttga gtgaagtagc ctaagaggat 2520
109 tcttttagaga atccgtattg aatttgtgtg gtatgtcact cagaaagaat cgtaatgggt 2580
111 atattgataa attttaaaat tggtatatatt gaaataaagt tgaatattat atataaaaaa 2640
113 aaaaaaaaaa aaa 2653
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117 <211> LENGTH: 750
118 <212> TYPE: PRT
119 <213> ORGANISM: Human
121 <400> SEQUENCE: 2
123 Met Trp Asn Leu Leu His Glu Thr Asp Ser Ala Val Ala Thr Ala Arg
124 1 5 10 15
127 Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly Gly Phe
128 20 25 30
131 Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser Ser Asn Glu
132 35 40 45
135 Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala Phe Leu Asp Glu
136 50 55 60
139 Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr Asn Phe Thr Gln Ile
140 65 70 75 80
143 Pro His Leu Ala Gly Thr Glu Gln Asn Phe Gln Leu Ala Lys Gln Ile
144 85 90 95
147 Gln Ser Gln Trp Lys Glu Phe Gly Leu Asp Ser Val Glu Leu Ala His
148 100 105 110
151 Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn Tyr Ile
152 115 120 125
155 Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile Phe Asn Thr Ser Leu Phe
156 130 135 140
159 Glu Pro Pro Pro Pro Gly Tyr Glu Asn Val Ser Asp Ile Val Pro Pro
160 145 150 155 160
163 Phe Ser Ala Phe Ser Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr
164 165 170 175
167 Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met
168 180 185 190
171 Lys Ile Asn Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val
172 195 200 205
175 Phe Arg Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly
176 210 215 220

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```

179 Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys
180 225                230                235                240
183 Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Gly Val Gln Arg Gly
184                245                250                255
187 Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro Gly Tyr
188                260                265                270
191 Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu Ala Val Gly
192                275                280                285
195 Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr Asp Ala Gln Lys
196                290                295                300
199 Leu Leu Glu Lys Met Gly Gly Ser Ala Pro Pro Asp Ser Ser Trp Arg
200 305                310                315                320
203 Gly Ser Leu Lys Val Pro Tyr Asn Val Gly Pro Gly Phe Thr Gly Asn
204                325                330                335
207 Phe Ser Thr Gln Lys Val Lys Met His Ile His Ser Thr Asn Glu Val
208                340                345                350
211 Thr Arg Ile Tyr Asn Val Ile Gly Thr Leu Arg Gly Ala Val Glu Pro
212                355                360                365
215 Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser Trp Val Phe Gly
216                370                375                380
219 Gly Ile Asp Pro Gln Ser Gly Ala Ala Val Val His Glu Ile Val Arg
220 385                390                395                400
223 Ser Phe Gly Thr Leu Lys Lys Glu Gly Trp Arg Pro Arg Arg Thr Ile
224                405                410                415
227 Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu Leu Gly Ser Thr
228                420                425                430
231 Glu Trp Ala Glu Glu Asn Ser Arg Leu Leu Gln Glu Arg Gly Val Ala
232                435                440                445
235 Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly Asn Tyr Thr Leu Arg Val
236                450                455                460
239 Asp Cys Thr Pro Leu Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu
240 465                470                475                480
243 Leu Lys Ser Pro Asp Glu Gly Phe Glu Gly Lys Ser Leu Tyr Glu Ser
244                485                490                495
247 Trp Thr Lys Lys Ser Pro Ser Pro Glu Phe Ser Gly Met Pro Arg Ile
248                500                505                510
251 Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu Val Phe Phe Gln Arg Leu
252                515                520                525
255 Lys Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn Trp Glu Thr Asn
256                530                535                540
259 Lys Phe Ser Gly Tyr Pro Leu Tyr His Ser Val Tyr Glu Thr Tyr Glu
260 545                550                555                560
263 Leu Val Glu Lys Phe Tyr Asp Pro Met Phe Lys Tyr His Leu Thr Val
264                565                570                575
267 Ala Gln Val Arg Gly Gly Met Val Phe Glu Leu Ala Asn Ser Ile Val
268                580                585                590
271 Leu Pro Phe Asp Cys Arg Asp Tyr Ala Val Val Leu Arg Lys Tyr Ala
272                595                600                605
275 Asp Lys Ile Tyr Ser Ile Ser Met Lys His Pro Gln Glu Met Lys Thr

```

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276      610      615      620
279 Tyr Ser Val Ser Phe Asp Ser Leu Phe Ser Ala Val Lys Asn Phe Thr
280 625      630      635      640
283 Glu Ile Ala Ser Lys Phe Ser Glu Arg Leu Gln Asp Phe Asp Lys Ser
284      645      650      655
287 Asn Pro Ile Val Leu Arg Met Met Asn Asp Gln Leu Met Phe Leu Glu
288      660      665      670
291 Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg
292      675      680      685
295 His Val Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser
296      690      695      700
299 Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp
300 705      710      715      720
303 Pro Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Tyr Val Ala Ala
304      725      730      735
307 Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala
308      740      745      750

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311 <210> SEQ ID NO: 3

312 <211> LENGTH: 8

313 <212> TYPE: PRT

314 <213> ORGANISM: Human

316 <400> SEQUENCE: 3

318 Ser Leu Tyr Glu Ser Trp Thr Lys

319 1 5

322 <210> SEQ ID NO: 4

323 <211> LENGTH: 15

324 <212> TYPE: PRT

325 <213> ORGANISM: Human

327 <220> FEATURE:

328 <221> NAME/KEY: MISC_FEATURE

329 <222> LOCATION: (6)..(7)

330 <223> OTHER INFORMATION: Xaa=unknown

333 <400> SEQUENCE: 4

W--> 335 Ser Tyr Pro Asp Gly Xaa Xaa Leu Pro Gly Gly Gly Val Gln Arg

336 1 5 10 15

339 <210> SEQ ID NO: 5

340 <211> LENGTH: 7

341 <212> TYPE: PRT

342 <213> ORGANISM: Human

344 <400> SEQUENCE: 5

346 Phe Tyr Asp Pro Met Phe Lys

347 1 5

350 <210> SEQ ID NO: 6

351 <211> LENGTH: 9

352 <212> TYPE: PRT

353 <213> ORGANISM: Human

355 <400> SEQUENCE: 6

357 Ile Tyr Asn Val Ile Gly Thr Leu Lys

358 1 5

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DATE: 08/07/2002

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Input Set : A:\1747-41426-A-PCT-US.txt

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361 <210> SEQ ID NO: 7
362 <211> LENGTH: 22
363 <212> TYPE: PRT
364 <213> ORGANISM: Human
366 <220> FEATURE:
367 <221> NAME/KEY: MISC_FEATURE
368 <222> LOCATION: (4)..(5)
369 <223> OTHER INFORMATION: Xaa=unknown
372 <400> SEQUENCE: 7
W--> 374 Phe Leu Tyr Xaa Xaa Thr Gln Ile Pro His Leu Ala Gly Thr Glu Gln
      375 1          5          10          15
      378 Asn Phe Gln Leu Ala Lys
      379          20
382 <210> SEQ ID NO: 8
383 <211> LENGTH: 17
384 <212> TYPE: PRT
385 <213> ORGANISM: Human
387 <400> SEQUENCE: 8
389 Gly Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Asp Val
      390 1          5          10          15
      393 Lys
397 <210> SEQ ID NO: 9
398 <211> LENGTH: 17
399 <212> TYPE: PRT
400 <213> ORGANISM: Human
402 <400> SEQUENCE: 9
404 Pro Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val
      405 1          5          10          15
      408 Lys
412 <210> SEQ ID NO: 10
413 <211> LENGTH: 15
414 <212> TYPE: PRT
415 <213> ORGANISM: Human
417 <400> SEQUENCE: 10
419 Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg
      420 1          5          10          15
423 <210> SEQ ID NO: 11
424 <211> LENGTH: 19
425 <212> TYPE: PRT
426 <213> ORGANISM: Human
428 <400> SEQUENCE: 11
430 Tyr Ala Gly Glu Ser Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile
      431 1          5          10          15
      434 Glu Ser Lys
438 <210> SEQ ID NO: 12
439 <211> LENGTH: 22
440 <212> TYPE: PRT
441 <213> ORGANISM: Human
443 <220> FEATURE:

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/08/403,803CDATE: 08/07/2002
TIME: 10:24:19Input Set : A:\1747-41426-A-PCT-US.txt
Output Set: N:\CRF3\08072002\H403803C.rawPlease Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; Xaa Pos. 6,7
Seq#:7; Xaa Pos. 4,5
Seq#:12; Xaa Pos. 14,15
Seq#:13; N Pos. 12
Seq#:14; N Pos. 6
Seq#:15; N Pos. 12
Seq#:16; N Pos. 6
Seq#:17; N Pos. 3,6
Seq#:18; N Pos. 11,15
Seq#:19; N Pos. 3
Seq#:20; N Pos. 18
Seq#:23; N Pos. 9
Seq#:24; N Pos. 12
Seq#:25; N Pos. 9
Seq#:26; N Pos. 9
Seq#:27; N Pos. 82,83,84,193,196,197,217,218,219,232,233,237,238,253,254
Seq#:27; N Pos. 255,256,263,600,601,721,722,723,724
Seq#:28; N Pos. 224,255,412,413,414,433,520,521,536,537,538,539,540,541,542
Seq#:28; N Pos. 543
Seq#:29; N Pos. 214,377